

## AMENDMENTS

### In the Title:

Please amend the title of the invention to read:

"PROCESS FOR SCREENING FOR HCV"

### In the Claims:

Please cancel claims 154-157, and 167.

Please add new claim 183.

H1  
183. A method according to any one of claims 123, 124 or 125, wherein the selected samples comprise antibodies that form an antigen-antibody complex with an amino acid sequence of at least 15 contiguous amino acids.

Please amend the following claims to read as follows:

H2  
SUB 2  
115. A method of selecting biological samples from a supply of biological samples comprising selecting from said supply those samples that contain a detectable polynucleotide comprising a contiguous sequence of at least 15 nucleotides fully complementary to either strand of Figure 3.

116. A method of selecting biological samples from a supply of biological samples comprising selecting from said supply those samples that contain a detectable polynucleotide comprising a contiguous sequence of at least 15 nucleotides fully complementary to either strand of Figure 62A.

117. A method of selecting biological samples from a supply of biological samples comprising selecting from said supply those samples that contain a detectable polynucleotide comprising a contiguous sequence of at least 15 nucleotides fully complementary to either strand of Figure 89.

H3 SUB 3  
118. A method of selecting biological samples from a supply of biological samples comprising selecting from said supply those samples that comprise either (i) a polynucleotide that hybridizes under stringent conditions to a polynucleotide that comprises a contiguous

sequence of at least 15 nucleotides from the genome of a hepatitis C virus genome or the complement thereof, or (ii) antibodies that form an antigen-antibody complex with an amino acid sequence of at least 10 contiguous amino acids encoded by a hepatitis C virus genome.

119. A method of selecting biological samples from a supply of biological samples comprising selecting from said supply those samples that comprise either (i) a polynucleotide that hybridizes under stringent conditions to a contiguous sequence of at least 15 nucleotides from either strand of at least one of the HCV cDNA inserts in a lambda gt-11 cDNA library deposited as ATCC No. 40394 or (ii) antibodies that form an antigen-antibody complex with an HCV polypeptide sequence of at least 10 contiguous amino acid encoded by an HCV cDNA insert in the lambda gt-11 library deposited as ATCC deposit No. 40394.

120. A method of selecting biological samples from a supply of biological samples comprising selecting from said supply those samples that comprise a polynucleotide that hybridizes under stringent conditions to a contiguous sequence of at least 15 nucleotides found in either strand of Figure 89.

121. A method of selecting biological samples from a supply of biological samples comprising selecting from said supply those samples that comprise a polynucleotide that hybridizes under stringent conditions to a contiguous sequence of at least 15 nucleotides found in either strand of Figure 14.

122. A method of selecting biological samples from a supply of biological samples comprising selecting from said supply those samples that comprise a polynucleotide that hybridizes under stringent conditions to a contiguous sequence of at least 15 nucleotides from either strand of at least one of the hepatitis C virus (HCV) cDNA inserts in a lambda gt-11 cDNA library deposited as ATCC No. 40394.

123. A method of selecting biological samples from a supply of biological samples comprising selecting from said supply those samples that comprise antibodies that form an

antigen-antibody complex with an amino acid sequence of at least 10 contiguous amino acids found in Figure 90.

124. A method of selecting biological samples from a supply of biological samples comprising selecting from said supply those samples that comprise antibodies that form an antigen-antibody complex with an amino acid sequence of at least 10 contiguous amino acids found in Figure 14.

125. A method of selecting biological samples from a supply of biological samples comprising selecting from said supply those samples that comprise antibodies that form an antigen-antibody complex with a hepatitis C virus (HCV) polypeptide sequence of at least 10 contiguous amino acid encoded by an HCV cDNA insert in [the] a lambda gt-11 library deposited as ATCC deposit No. 40394.

126. A method according to any of claims 118-122 wherein said selected samples comprise said polynucleotide and said stringent conditions permit the formation of a stable hybrid duplex between said polynucleotide and said contiguous sequence and do not permit the formation of a stable duplex between said contiguous sequence and the genomes of Hepatitis B or Hepatitis A viruses.

127. A method according to claim 132 further comprising preparing polyclonal antibodies with the selected biological samples.

128. A method according to claim 133 further comprising preparing polyclonal antibodies with the selected biological samples.

129. A method according to claim 138 further comprising preparing polyclonal antibodies with the selected biological samples.

130. A method according to claim 142 further comprising preparing polyclonal antibodies with the selected biological samples.

131. A method of selecting biological samples from a supply of biological samples comprising selecting from said supply those samples that contain a detectable polynucleotide

comprising a sequence that is fully complementary to a contiguous sequence of at least 15 nucleotides from the genome of a hepatitis C virus genome or the complement thereof.

163. A method of selecting biological samples from a supply of biological samples comprising selecting from said supply those samples that contain a detectable polynucleotide comprising a sequence that is fully complementary to a contiguous sequence of at least 15 nucleotides from either strand of at least one of the HCV cDNA inserts in a lambda gt-11 cDNA library deposited as ATCC No. 40394.

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